

OM of: US-09-294-298-2 to: GenEmbl:* out_format : pfs

Date: Jan 19, 2001 12:18 AM

About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09294298/runat_17012001_125501_27756/app_query.fasta_1.4359
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09294298 @CGN1_1_13912 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY-WAIT -THREADS=1
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Search information block:

Query: US-09-294-298-2

Query length: 1423

Database: GenEmbl: ★

Database sequences: 1118133

Database length: -1736092196

Search time (sec): 10440.680000

score_list:	Strd Orig	zScore	Escore	Len	Documentation	..
gb_ro:AF058789	+ 7451.00	3007.46	2.3e-159	4539	! AF058789	Rattus norvegicus Syn
gb_ro:AF058790	+ 7057.50	2850.18	1.3e-150	4140	! AF058790	Rattus norvegicus Syn
gb_ro:AF050183	+ 6894.00	2784.46	6.1e-147	4265	! AF050183	Rattus norvegicus GTE
gb_ro:AF048976	+ 6885.50	2781.31	7.9e-147	4063	! AF048976	Rattus norvegicus syn
gb_ro:AB016962	+ 6309.50	2549.08	7.9e-134	4801	! AB016962	Rattus norvegicus mRNA
gb_htg20:AL161903	+ 4064.00	1630.85	1.1e-82	150956	! AL161903	Homo sapiens Chrom
gb_pr7:HS0570F3	- 4059.50	1631.51	1.0e-82	94770	! AL050332	Human DNA sequence
gb_htg20:AL161906	+ 3987.00	1599.36	6.3e-81	169323	! AL161906	Homo sapiens chromo
gb_pr3:AF047711	+ 2620.50	1070.88	1.7e-51	4368	! AF047711	Homo sapiens nGAP mRNA
gb_htg7:AC019800	- 1257.50	510.81	2.7e-20	56366	! AC019800	Drosophila melanog
gb_htg4:AC012162	+ 1257.50	504.32	6.2e-20	191504	! AC012162	Drosophila melanog
gb_htg4:AC012161	- 1257.50	504.02	6.5e-20	202741	! AC012161	Drosophila melanog
gb_in1:AE003506	+ 1257.50	501.92	8.4e-20	300994	! AE003506	Drosophila melanog
gb_in1:AB011280	+ 1201.00	502.22	8.1e-20	3984	! AB011280	Caenorhabditis eleg
gb_htg6:AC016523	+ 1092.50	443.82	1.5e-16	65961	! AC016523	Drosophila melanog
gb_pr4:AK022662	+ 1088.50	459.84	1.9e-17	2385	! AK022662	Homo sapiens cDNA FLJ
gb_pr4:AK024488	+ 1080.50	453.52	4.1e-17	4287	! AK024488	Homo sapiens mRNA for
gb_ro:AF053938	+ 906.00	392.28	1.1e-13	829	! AF053938	Rattus norvegicus p135
gb_htg22:AL365274	- 710.00	285.37	9.7e-08	172027	! AL365274	Homo sapiens chromo
gb_in2:CEC07B5	+ 676.50	279.73	2.0e-07	39660	! Z46266	Caenorhabditis eleg
gb_pr6:HS593C16	- 650.50	265.45	1.3e-06	81971	! AL035702	Human DNA sequence
gb_htg12:AC027051	+ 650.50	262.01	1.9e-06	156700	! AC027051	Homo sapiens chromo
gb_htg3:AC011492	+ 613.00	246.94	1.3e-05	157803	! AC011492	Homo sapiens chromo
gb_htg17:AC073765	+ 600.00	239.55	3.5e-05	237619	! AC073765	Mus musculus clone
gb_in1:AB011279	+ 531.00	236.56	5.1e-05	2276	! AB011279	Caenorhabditis eleg
gb_htg3:AC011703	+ 502.00	202.36	0.0041	159777	! AC011703	Drosophila melanog
gb_pr1:AB011110	+ 488.50	214.76	0.0008	5579	! AB011110	Homo sapiens mRNA for
gb_htg13:AC040900	+ 479.50	193.49	0.0128	155332	! AC040900	Homo sapiens chromo
gb_htg20:AL161906	- 479.00	192.83	0.0139	169323	! AL161906	Homo sapiens chromo
gb_ro:RATGAPX	+ 455.00	204.12	0.0033	3296	! L13151	Rat GTPase-activating
gb_pr8:HUMGAPB	+ 437.50	196.85	0.0083	3456	! M23612	Human GTPase-activating
gb_pr8:HUMGAPA	+ 437.50	195.68	0.0096	4307	! M23379	Human GTPase-activating
gb_om:BTGAPR	+ 433.50	193.88	0.0121	4473	! X12602	Bovine mRNA for GTPase
gb_om:BTU30857	+ 431.00	195.50	0.0099	2730	! U30857	Bos taurus R-Ras GTPase
gb_pl2:BGR27158	+ 430.50	194.55	0.0111	3144	! AJ272158	Blumeria graminis f.
gb_pat1:EL3125	+ 429.50	195.06	0.0104	2647	! E13125	Bovine gene for R-Ras
gb_in3:DME012609	+ 420.00	189.77	0.0206	3502	! AJ012609	Drosophila melanogast
gb_htg12:AC027051	- 417.00	168.39	0.0395	156700	! AC027051	Homo sapiens chromo
gb_in1:AB011283	+ 395.50	188.05	0.0256	760	! AB011283	Caenorhabditis elegans
gb_pr4:AK026441	+ 394.50	180.71	0.0658	2813	! AK026441	Homo sapiens cDNA: FI
gb_pr4:HSIN034BP	+ 381.00	175.25	0.1325	2837	! X89399	Homo sapiens mRNA for

Percent Similarity: 98.001 Percent Identity: 98.001
alignment_block:
US-09-294-298-2 x AF058789 ..
Align seg 1/1 to: AF058789 from: 1 to: 4539

1 MetSerTyrAlaProPheArgAspValArgGlyProProMetHisArgTh 17
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1 ATGTCCCTATGCCCCCTTCAGAGATGTACGGGGACCCCTATGCACCGAAC 50

17 rGlnTyrValHisSerProTyrAspArgProGlyTrpAsnProArgPheC 34
|||||
51 CCAATACGTTTCATTCCTCCCGTATGACCGTCCCGGTTGGAAACCCCGGTTCT 100

34 ysIleIleSerGlyAsnGlnLeuLeuMetLeuAspGluAspGluIleHis 50
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101 GCATCATCTCTGGGAACACAGCTGCTCATGCTGGATGAGGATGAGATACAC 150

51 ProLeuLeuIleArgAspArgArgSerGluSerSerArgAsnLysLeuLe 67
|||||
151 CCCCTTCTGTATCCCGCGACCGGAGGAGCGAGTCCAGCCGGAACAAACTGCT 200

67 uArgArgThrValSerValProValGluGlyArgProHisGlyGluHisG 84
|||||
201 GAGACGCACCGTCTCTGTGCCAGTGGAGGGCGGCCCCACGCGGAGCATG 250

84 luTyrHisLeuGlyArgSerArgArgLysSerValProGlyGlyLysGln 100
|||||
251 AATACCACTTGGGTCGCTCGAGGAGGAAGAGTGTCCCCGGGGGGAACAG 300

101 TyrSerMetGluAlaAlaProAlaAlaPropheArgProSerGlnGlyph 117
|||||
301 TACAGCATGGAAGCCGCCCGCTGCGCCCTTCCGGGCCCTCGAAGGCTT 350

117 eLeuSerArgArgLeuLysSerSerIleLysArgThrLysSerGlnProL 134
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351 CCTGAGCCGGAGGCTAAAAAGCTCCATCAAACGTTACAAAGTCAACAACCCA 400

134 ysLeuAspArgThrSerSerPheArgGlnIleLeuProArgPheArgSer 150
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401 AACTTGACCGGACCAAGAGCTTTCGACAGATCCTGCCTCGCTTCCGAAGT 450

151 AlaAspHisAspArgAlaArgLeuMetGlnSerPheLysGluSerHisSe 167
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451 GCTGACCATGACCGGCCGCTGATGCAGAGCTTCAAGGAGTCTCACTC 500

167 rHisGluSerLeuLeuSerProSerSerAlaAlaGluAlaLeuGluLeuA 184
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501 CCATGAGTCCCTGCTGAGTCCAGCAGTGTCTGTGAGGCCCTGGAGCTCA 550

184 snLeuAspGluAspSerIleIleLysProValHisSerSerIleLeuGly 200
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551 ACCTGGATGAAGACTCCATTATCAAGCCAGTACACAGCTCCATCCTGGGC 600

201 GlnGluPheCysPheGluValThrThrSerSerGlyThrLysCysPheAl 217
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601 CAGGAGTTCGTCTTGAGGTAACAACATCGTCTGGGACAAAATGTTTTCG 650

217 aCysArgSerAlaAlaGluArgAspLysTrpIleGluAsnLeuGlnArgA 234
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651 CTGTGGTCTGCAGCCGAAAGGGACAAATGGATTGAGAAATCTACAGAGG 700

234 laValLysProAsnLysAspAsnSerArgArgValAspAsnValLeuLys 250
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701 CTGTGAAACCCCAACAGGACAAACAGCCGCGGCTAGATAACGTGCTGAAA 750

251 LeuTrpIleIleGluAlaArgGluLeuProProLysLysArgTyrTyrCy 267
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751 CTATGGATCATAGAGCTCGAGAGCTGCCCCCAAGAAGCGGATATTACTG 800

267 sGluLeuCysLeuAspAspMetLeuTyrAlaArgThrThrSerLysProA 284
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801 CGAGTTATGCCTGGACGACATGCTCTATGACGGACCACCTTCCAAGCCCC 850

284 rgSerAlaSerGlyAspThrValPheTrpGlyGluHisPheGluPheAsn 300
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351 ThrLeuProThrGlySerGlySerGlyMetGlySerGlyGlyGlyGlyG 367
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367 yGlyGlySerGlyGlySerGlyLysGlyLysGlyLysGlyCysProA 384
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384 laValArgLeuLysAlaArgTyrGlnThrMetSerIleLeuProMetGlu 400
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1151 CTGTGGCGCTCAAGGCCCGCTTACCAGACAATGAGTATCCTGCCCATGGAG 1200

401 LeuTyrLysGluPheAlaGluTyrValThrAsnHisTyrArgMetLeuC 417
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1201 CTATATAAGGAGTTTGCAGAAATATGTACCAACCACTACCGCATGCTGTG 1250

417 sAlaValLeuGluProAlaLeuAsnValLysGlyLysGluGluValAlas 434
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1251 TGCCGTGCTGGAGCCCGCCCTCAATGTCAAGGGCAAGGAGGTCGCTA 1300

434 erAlaLeuValHisIleLeuGlnSerThrGlyLysAlaLysAspPheLeu 450
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1301 GTGCACCTGGTTCACATCCTGCAAAAGCACAGGCAAGGCCAAGGACTTCCTT 1350

451 SerAspMetAlaMetSerGluValAspArgPheMetGluArgGluHisLe 467
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1351 TCAGACATGGCCATGTGAGAGGTAGACCGGTTTCATGGAGCGGGAACACCT 1400

467 uIlePheArgGluAsnThrLeuAlaThrLysAlaIleGluGluTyrMeta 484
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1401 CATATTCCGCGAGAACACGCTCGCCACTAAAGCCATAGAAAGTATATGA 1450

484 rgLeuIleGlyGlnLysTyrLeuLysAspAlaIleGlyGluPheIleArg 500
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1451 GACTGATTGGCCAGAAATACCTCAAGGATGCCATTGGGAGATTTCATCCGG 1500

501 AlaLeuTyrGluSerGluGluAsnCysGluValAspProIleLysCysTh 517
|||||
1501 GCTCTGTATGAATCTGAGGAGAACTGTGAAGTAGACCCCATCAAGTGAC 1550

517 rAlaSerSerLeuAlaGluHisGlnAlaAsnLeuArgMetCysCysGluL 534
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1551 AGCCTCCAGTCTGGCAGAGCACCAAGGCCAACCTGCGGATGTGCTGTGAGT 1600

534 euAlaLeuCysLysValValAsnSerHisCysValPheProArgGluLeu 550
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551 LysGluValPheAlaSerTrpArgLeuArgCysAlaGluArgGlyArgGl 567
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567 uAspIleAlaAspArgLeuIleSerAlaSerLeuPheLeuArgPheLeuC 584
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584 ysProAlaIleMetSerProSerLeuPheGlyLeuMetGlnGluTyrPro 600
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 651 GluIleSerAsnLeuAspThrLeuThrAsnSerSerPheGluGlyTy 667
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 667 rIleAspLeuGlyArgGluLeuSerThrLeuHisAlaLeuLeuTyrGluV 684
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 2451 GAAGATGCTGAGTGTCAACAAGAGTGTGTCCATGCTGGACCTGCAGGGCG 2500
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 3001 GATTTTACCGTCGGCAGCTCTCTACAGGGGTCCCTAAGCCCGCTCGGCCT 3050
 1017 uSerProProGlnIleThrIleGlyProGlnArgProAlaProSerGlyP 1034
 3051 CTCCCGCCCGCAGATCACCATCGGTCCCGCAGAGGCCAGCTCCCTCAGGGC 3100
 1034 roGlyGlySerGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlnPro 1050
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 1084 yrglyProAlaArgProArgGlnGlnSerLeuSerLysGlySerIle 1100
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 3351 CATCACCAGCAGCATTCACAGACTCCATCCACGCTGAACCCACCATGTC 3400
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 1151 AlaAspIleGluSerAlaHisIleGluArgGluGluTyrLysLeuLysGl 1167
 3451 GCTGACATCGAGAGTGCACACATTGAGCGGGGAGAGTACAAGCTGAAGGA 3500
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 3501 GTACTCGAAGTCCATGGACGAGAGCGGAGTGGACAGGGGTGAAGGAGTACG 3550
 1184 luGluGluIleHisSerLeuLysGluArgLeuHisMetSerAsnArgLys 1200

61 SerSerArgAsnLysLeuLeuArgArgThrValSerValProValGluG1 77
 67 TCCACCGCCAGCCTCTCCGCGCGCGCTGCTCTTCCCTGCTGCTTCCGGG 116
 77 yArgProHisGlyGluHisGluTyrHisLeuGlyArgSerArgArgLys 94
 117 G.....GAATACCACTTGGTGGCTCGAGGAGGAAGA 148
 94 erValProGlyGlyLysGlnTyrSerMetGluAlaAlaProAlaPro 110
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 111 PheArgProSerGlnGlyPheLeuSerArgArgLeuLysSerSerileLy 127
 199 TTCCGGCCCTCGCAAGGCTTCCGTGACCGGAGGCTAAAGAGCTCCATCA 248
 127 sArgThrLysSerGlnProLysLeuAspArgThrSerSerPheArgGlnI 144
 249 ACGTACAAAGTCAACCCAACTTGACCGGACCGAGCTTTCGACAGA 298
 144 leLeuProArgPheArgSerAlaAspHisAspArgAlaArgLeuMetGln 160
 299 TCCTGCCTCGCTCCGAAGTGTGACCATGACCGGCGCGCGCTGATGCG 348
 161 SerPheLysGluSerHisSerHisGluSerLeuLeuSerProSerSerAl 177
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 194 alHisSerSerileLeuGlyGlnGluPheCysPheGluValThrThrSer 210
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 227 pileGluAsnLeuGlnArgAlaValLysProAsnLysAspAsnSerArg 244
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 244 rgValAspAsnValLeuLysLeuTrpIleIleGluAlaArgGluLeupro 260
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 261 ProLysLysArgTyrTyrCysGluLeuCysLeuAspAspMetLeuTyrAl 277
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 949 GGTATGGGCTCGGGGGAGGAGGGGGTTCAGGGGGGGCTCAGGGGGCAA 998
 377 sGlyLysGlyGlyCysProAlaValArgLeuLysAlaArgTyrGlnThrM 394
 999 AGGAAAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
 394 etSerileLeuPrometGluLeuTyrLysGluPheAlaGluTyrValThr 410
 1049 TGAGTATCCTGCCCATGGAGCTATATAAGGAGTTGCAGAAATATGTGACC 1098
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 1099 AACCACTACCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1148
 427 sGlyLysGluGluValAlaSerAlaLeuValHisIleLeuGlnSerThrG 444
 1149 GGGCAAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1198
 444 lyLysAlaLysAspPheLeuSerAspMetAlaMetSerGluValAspArg 460
 1199 GCAAGCCCAAGGACTTCTTTCAGACATGGCCATGTCTAGAGGTAGACCGG 1248
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 1249 TTCATGGAGCGGGAAACACCTCATATTTCCCGGAGAGACACGCTCGCCACTAA 1298
 477 sAlaIleGluGluTyrMetArgLeuIleGlyGlnLysTyrLeuLysAspA 494
 1299 AGCCATAGAAGAGTATATGAGACTGATTGGCCAGAAATACCTCAAGGATG 1348
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 511 ValAspProIleLysCysThrAlaSerSerLeuAlaGluHisGlnAlaAs 527
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 527 nLeuArgMetCysCysGluLeuAlaLeuCysLysValValAsnSerHisC 544
 1449 CCTGCGATGTGCTGTGAGTTGGCCCTGTGCAAGGTGGTCAACTCCCAT 1498
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REFERENCE 1 (bases 1 to 4265)
AUTHORS Kim, J.H., Liao, D., Lau, L.F. and Haganir, R.L.
TITLE Syngap1: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family
JOURNAL Neuron 20 (4), 683-691 (1998)
MEDLINE 98240917
REFERENCE 2 (bases 1 to 4265)
AUTHORS Kim, J.H. and Haganir, R.L.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1998) Neuroscience, Johns Hopkins Medical Institute, 725 N. Wolfe Street, PCTB 900, Baltimore, MD 21205, USA
COMMENT On Sep 15, 2000 this sequence version replaced gi:3044054.
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DEFINITION Rattus norvegicus synaptic ras GTPase-activating protein p135
SYNGAP mRNA, complete cds.

ACCESSION AF048976
VERSION AF048976.1 GI:2935447

KEYWORDS

SOURCE

ORGANISM

Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 4063)
Chen, H.-J. and Kennedy, M.B.
Identification and cloning of a novel 130 kD protein containing a
ras GTPase-activating domain from the rat forebrain postsynaptic
density.

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REFERENCE
AUTHORS
TITLE
(Int) SOC. NEUROSCI. ABSTR.: 1466; (1997)
2 (bases 1 to 4063)
Chen, H.-J., Rojas-Soto, M., and Kennedy, M.B.
A synaptic Ras GTPase-activating protein (p135 SynGAP) inhibited by
Cam kinase II.

JOURNAL

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AUTHORS

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Backhand date

Seq ID
No 2

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LOCUS AB016962 4801 bp mRNA ROD 01-SEP-2000

DEFINITION Rattus norvegicus mRNA for synGAP-d, complete cds.

ACCESSION AB016962

VERSION AB016962.1 GI:4417206

KEYWORDS synGAP-b1.

SOURCE Rattus norvegicus (sub_species:Sprague Dawley) cDNA to mRNA.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 4801)

AUTHORS Suzuki,T.

TITLE SynGAP-d

JOURNAL Published Only in DataBase (1999) In press

REFERENCE 2 (bases 1 to 4801)

AUTHORS Suzuki,T.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo

Suzuki, Shinshu University School of Medicine, Department of

Neuroplasticity; 3-1-1 Asahi, Matsumoto, Nagano 390-8621, Japan

(E-mail:suzukitesch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683,

Fax:+81-263-37-2725)

COMMENT On Mar 16, 1999 this sequence version replaced gi:4239945.

Sequence updated (09-Feb-1999).

FEATURES Location/Qualifiers

source

1. .4801

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1424 TTCTGCTTTGAGGTAACAACATCGTCTGGGACAAAATGTTTTCCTGTGC 1473

219 gSerAlaAlaGluArgAspLysTrpIleGluAsnLeuGlnArgAlaValL 236
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1474 GTCTGCAGCCGAAAGGACAAAATGGATTGAGAAATCTACAGAGGGCTGTGA 1523
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236 ysProAsnLysAspAsnSerArgArgValAspAsnValLeuLysLeuTrp 252
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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319 sArgLysLysAspLysAlaGlyTyrValGlyLeuValThrValProVala 336
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1774 GCGGAAGAAGGACAAGCAGGCTACGTTGGCTGGTGACTGTTCCAGTGG 1823

336 laThrLeuAlaGlyArgHisPheThrGluGlnTrpTyrProValThrLeu 352
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1824 CCACCCTGGCTGGCGCCACTTTCACAGAGCACTGTACCCCGTGACCCTG 1873

353 ProThrGlySerGlyGlySerGlyGlyMetGlySerGlyGlyGlyGlyG1 369
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1874 CCAACAGGAAGTGGGGCTCTGGGGGTATGGGCTCGGGGGGAGGAGGGG 1923

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386 rgLeuLysAlaArgTyrGlnThrMetSerIleLeuProMetGluLeuTyr 402
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586 laIleMetSerProSerLeuPheGlyLeuMetGlnGluTyrProAspGlu 602
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653 SerAsnLeuAspThrLeuThrAsnSerSerSerPheGluGlyTyrIleAs 669
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2774 TCCAACCTGGACACACTGACCAACAGCAGCAGTTTGTAGGGCTACATAGA 2823

669 pLeuGlyArgGluLeuSerThrLeuHisAlaLeuLeuTrpGluValLeuP 686
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2824 CTTGGGCCGCGAGCTCTCCACACTTCACGCCCTGCTCTGGGAGTGCTGC 2873

686 roGlnLeuSerLysGluAlaLeuLeuLysLeuGlyProLeuProArgLeu 702
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2874 CCCAGCTCAGCAAGGAAGCCCTCCTGAAGCTGGCCCGCTGCCCGGGCTC 2923

703 LeuSerAspIleSerThrAlaLeuArgAsnProAsnIleGlnArgGlnPr 719
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719 oSerArgGlnSerGluArgAlaArgSerGlnProMetValLeuArgGlyP 736
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ACCESSION  AL161903
VERSION    AL161903.12  GI:10039702
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 150956)
AUTHORS   Tracey,A.
TITLE     Direct Submission
JOURNAL   Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT   On Sep 9, 2000 this sequence version replaced gi:9796876.
            ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: bA175A4

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----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 145680 bases at least Q40
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Insert size: 150756; sum-of-contigs
Insert size: 148326; 10.8% error; agarose-fp
Quality coverage: 6.43x in Q20 bases; sum-of-contigs Quality
coverage: 6.54x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 54611: contig of 54611 bp in length
*      54612 54711: gap of 100 bp
*      54712 70293: contig of 15582 bp in length
*      70294 70393: gap of 100 bp
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BASE COUNT           39575 a 37381 c 36411 g 37389 t   200 others
ORIGIN

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    Ratio: 3.827              Gaps: 22
    Percent Similarity: 32.869  Percent Identity: 31.848

alignment_block:
US-09-294-298-2 x ALL161903/rev ..

Align seg 1/1 to reverse of: ALL161903 from: 1 to: 150956

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OM of: US-09-294-298-2 to: Issued_Patents_NA:* out_format : pfs
Date: Jan 19, 2001 7:43 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
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Search information block:
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Query length: 1423
Database: Issued_Patents_NA:*
Database sequences: 280836
Database length: 80580151
Search time (sec): 156.930000

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/cgn2_6/ptodata/2/ina/PCRTUS_COMB.seq:PCT-US93-04102-1 + 239.00 224.40 6.0e-05 42
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seq_documentation_block:
; Sequence 24, Application US/08190687B
; Patent No. 5760203
; GENERAL INFORMATION:
; APPLICANT: Wong, Gail L.
; APPLICANT: Martin, George
; APPLICANT: McCormick, Francis P.
; APPLICANT: Rubinfeld, Bonnie
; APPLICANT: O'Rourke, Edward C.
; APPLICANT: Clark, Robin
; TITLE OF INVENTION: GAP Gene Sequences
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,687B
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/774,644
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/260,807
; FILING DATE: 21-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/230,761
; FILING DATE: 10-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27527/31898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3456 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..2709
; US-08-190-687B-24
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Quality: 437.50 Length: 568
Ratio: 1.326 Gaps: 22
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US-09-294-298-2 x US-08-190-687B-24 ..

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seq_documentation_block:

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XX

AC Q10988;

XX
DT 22-MAY-1991 (first entry)

OM of: US-09-294-298-2 to: EST:* out_format : pfs

Date: Jan 18, 2001 9:24 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09294298/runat_17012001_125501_27745/app_query.fasta_1.4359
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US09294298@cgnl_1_7119 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-294-298-2

Query length: 1423

Database: EST:*

Database sequences: 7991742

Database length: ~791223438

Search time (sec): 4688.750000

score_list:	Sequence	Strtd	Orig	Zscore	EScore	Len	Documentation
	gb_est37:AV590698	+	933.00	1072.14	1.0e-50	571	! AV590698 AV590698 Bos taurus br
	gb_gss21:AZ399131	-	764.00	879.28	5.8e-40	474	! AZ399131 LM0164P14R Mouse 10kb
	gb_est49:AW779747	-	737.50	846.16	4.0e-38	593	! AW779747 hn85f10.x1 NCI_CGAP_Ki
	gb_est44:AW421227	-	731.50	839.16	9.9e-38	597	! AW421227 fj94f10.x1 zebrafish g
	gb_est71:BE490923	-	706.00	809.16	4.6e-36	628	! BE490923 db38g08.x1 Blackshear/
	gb_est22:AI606711	+	660.00	757.27	3.6e-33	566	! AI606711 ml58d01.y1 Stratagene
	gb_est71:BE463433	-	628.50	723.22	2.8e-31	463	! BE463433 hw23d06.x1 NCI_CGAP_Ki
	gb_est22:AI577567	-	600.00	689.22	2.2e-29	511	! AI577567 UI-R-Y0-vk-d-04-0-UI.s
	gb_est41:AW205989	-	571.50	657.19	1.4e-27	474	! AW205989 UI-H-B11-afy-d-12-0-UI
	gb_est28:AJ396547	+	566.50	646.86	5.1e-27	707	! AJ396547 AJ396547 dkfz426 Gallu
	gb_est11:AA709010	-	563.00	648.57	4.1e-27	427	! AA709010 zf94hl1.s1 Soares_pine
	gb_est22:AI609604	-	548.50	631.00	3.9e-26	460	! AI609604 tw91e09.x1 NCI_CGAP_HN
	gb_est9:AA554056	-	543.50	625.50	7.9e-26	449	! AA554056 nl01g07.s1 NCI_CGAP_Cc
	gb_est27:AI958829	+	537.50	616.17	2.6e-25	555	! AI958829 fd22g01.y1 Zebrafish w
	gb_est40:AW136165	-	531.50	611.81	4.6e-25	443	! AW136165 UI-H-B11-abz-d-09-0-UI
	gb_est9:AA554055	-	517.50	595.43	3.7e-24	452	! AA554055 nl01g06.s1 NCI_CGAP_Cc
	gb_est10:AA691827	+	504.00	580.88	2.4e-23	413	! AA691827 vt05d01.r1 Barstead m
	gb_gss26:CNS02VGW	+	501.00	567.12	1.4e-22	1020	! AL215753 Tetraodon nigroviridis
	gb_est74:BE695645	+	486.00	557.58	4.8e-22	516	! BE695645 MR1-BT0800-030700-002-
	gb_est9:AA575948	-	484.50	559.37	3.8e-22	379	! AA575948 nm56e05.s1 NCI_CGAP_Br
	gb_est22:AI562171	-	484.50	559.28	3.9e-22	382	! AI562171 vw73f04.x1 Stratagene
	gb_est41:AW204612	-	481.00	556.33	5.6e-22	347	! AW204612 UI-H-B11-aej-c-02-0-UI
	gb_est39:AW076911	+	473.00	547.17	1.8e-21	345	! AW076911 fj03d08.y1 Zebrafish a
	gb_est76:BE848541	+	464.00	530.55	1.5e-20	596	! BE848541 uw39f05.y1 Soares_thym
	gb_gss26:CNS02JDV	+	461.50	522.01	4.6e-20	979	! AL200092 Tetraodon nigroviridis
	gb_gss26:CNS02JJK	-	457.50	519.25	6.5e-20	832	! AL200329 Tetraodon nigroviridis
	gb_gss14:AQ993964	+	454.00	517.48	8.2e-20	682	! AQ993964 RPCI-23-241C10.TV RPCI
	gb_gss26:CNS01XQ5	+	452.50	516.64	9.1e-20	631	! AL172022 Tetraodon nigroviridis
	gb_gss25:CNS00HWF	-	425.50	480.17	9.8e-18	1006	! AL073826 Drosophila melanogast
	gb_gss26:CNS03ANH	+	419.50	473.60	2.3e-17	975	! AL235430 Tetraodon nigroviridis
	gb_est45:AW527364	-	418.50	485.26	5.1e-18	317	! AW527364 UI-R-B01-ajj-e-01-0-UI
	gb_est59:BB321064	+	417.50	482.56	7.2e-18	363	! BB321064 BB321064 RIKEN full-1e
	gb_est26:AI874961	-	416.50	482.29	7.5e-18	336	! AI874961 ul27f03.x1 Sugano mous
	gb_gss27:CNS04DL0	+	416.50	471.35	3.0e-17	877	! AL285885 Tetraodon nigroviridis
	gb_est4:AA258366	-	401.50	465.57	6.4e-17	319	! AA258366 zr59e01.s1 Soares_NhM
	gb_gss27:CNS041WW	+	401.00	452.85	3.3e-16	926	! AL270761 Tetraodon nigroviridis
	gb_est47:AW565799	+	394.00	450.88	4.2e-16	542	! AW565799 109245 MARC 1BOV Bos t
	gb_est61:BB394547	+	383.50	444.59	9.4e-16	325	! BB394547 BB394547 RIKEN full-1e
	gb_est23:AI650331	+	379.00	440.47	1.6e-15	296	! AI650331 wa18f01.x1 NCI_CGAP_Ki
	gb_est14:AA953060	-	368.50	428.51	7.4e-15	292	! AA953060 oo01g09.s1 Soares_NFL

gb_est59:BB312776 + 365.50 424.40 1.3e-14 309 ! BB312776 BB312776 RIKEN full
gb_est75:BE773015 - 365.50 419.36 2.4e-14 481 ! BE773015 KC1-FT0134-170700-0
gb_est19:AI327335 - 358.00 407.25 1.1e-13 651 ! AI327335 mp74cl1.x1 Soares_t
gb_est66:BE085114 - 357.50 414.25 4.6e-14 335 ! BE085114 CM2-BT0664-240200-1

seq_name: gb_est37:AV590698

seq_documentation_block:
LOCUS AV590698 571 bp mRNA EST 29-AUG-2000
DEFINITION AV590698 Bos taurus brain fetus Bos taurus cDNA clone E1BR014B04
5', mRNA sequence.

ACCESSION AV590698
VERSION AV590698.1 GI:9701691
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 571)
AUTHORS Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
Suzuki,H.

TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division

Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES
Location/Qualifiers

1..571
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="E1BR014B04"
/clone_lib="Bos taurus brain fetus"
/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 124 a 161 c 169 g 116 t 1 others
ORIGIN

alignment_scores:
Quality: 933.00 Length: 186
Ratio: 5.043 Gaps: 1
Percent Similarity: 99.462 Percent Identity: 99.462

alignment_block:
US-09-294-298-2 x AV590698 ..

Align seg 1/1 to: AV590698 from: 1 to: 571

429 LysGluGluValAlaSerAlaLeuValHisIleLeuGlnSerThrGlyLy 445
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13 AAGGAGGAGGTCGCCAGTGCTCTGGTTCACATCCTGCAGAGTACAGGCAA 62
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445 sAlaLysAspPheLeuSerAspMetAlaMetSerGluValAspArgPheM 462
|||||

63 GGCCAAGGACTTCCTTTTCAGACATGGCCATGTCCGAGGTGGACCGGTTCA 112
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462 etGluArgGluHisLeuIlePheArgGluAsnThrLeuAlaThrLysAla 478
|||||

113 TGGAACGAGAACACCTCATATTCCGCGAGAACACGCTCGCCACTAAAGCC 162
|||||

479 IleGluGluTyrMetArgLeuIleGlyGlnLysTyrLeuLysAspAlaI 495
|||||

163 ATAGAAGAGTACATGAGACTGATTGGTCAGAAATACCTCAAGGATGCCAT 212
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495 eGlyGluPheIleArgAlaLeuTyrGluSerGluGluAsnCysGluValA 512
|||||
213 CGGGGAATTCATCGTGCTCTGTATGAATCTGAGGAGAACTGTGAGGTGG 262
|||||
512 spProfileLysCysThrAlaSerSerLeuAlaGluHisGlnAlaAsnLeu 528
|||||
263 ACCCATCAAGTGCACGGCATCCAGTTTGGCTGAGCACCAGGCCAACCTG 312
|||||
529 ArgMetCysCysGluLeuAlaLeuCysLysValValAsnSerHisCysVa 545
|||||
313 CGGATGTGCTGTGAGTTGGCCCTGTGCAAGGTGGTCAACTCCCATTCGCT 362
|||||
545 lPheProArgGluLeuLysGluValPheAlaSerTrpArgLeuArgCysA 562
|||||
363 GTTCCCGAGGGAGCTGAAGGAGGTGTTCGTCCTGCGGACTGCGCTGTG 412
|||||
562 laGluArgGlyArgGluAspIleAlaAspArgLeuIleSerAlaSerLeu 578
|||||
413 CAGAGCGGGCCGAGAGGACATTGCGGACCGGCTGATCAGCGCCTCGCTC 462
|||||
579 PheLeuArgPheLeuCysProAlaIleMetSerProSerLeuPhe.GlyL 595
|||||
463 TTCCTGCGCTTCTCTGCGCGCCATTATGTGCGCCAGCCTNTTCGGGGC 512
|||||
595 euMetGlnGluTyrProAspGluGlnThrSerArgThrLeuThrLeuIle 611
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513 TCATGCAGGAGTACCCAGATGAGCAAACTTCGAGAAACCTCAGCGCTCATC 562
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612 AlaLys 613
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563 GCCAAG 568
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seq_name: gb_gss21:AZ399131

seq_documentation_block: 474 bp DNA GSS 03-OCT-2000
LOCUS AZ399131
DEFINITION IM0164P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0164P14 R, DNA sequence.
ACCESSION AZ399131
VERSION AZ399131.1 GI:10514203
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 474)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0164 row: P column: 14
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Class: plasmid ends
High quality sequence stop: 474.
Location/Qualifiers
1 .474
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/strain="C57BL/6J"
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FEATURES
source
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|47321141|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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BASE COUNT 92 a 151 c 131 g 100 t
ORIGIN
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Percent Similarity: 100.000 Percent Identity: 99.296
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US-09-294-298-2 x AZ399131/rev ..
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426 CAGGACAACAGCCCGCGAGTAGATAACGTGCTGAAGCTATGGATCATAGA 377
|||||
255 uAlaArgGluLeuProProLysLysArgTyrTyrCysGluLeuCysLeuA 272
|||||
376 GGCTCGAGAGCTGCCCCCAAGAAGAGATATTACTGTGAGCTGTGCCCTGG 327
|||||
272 spAspMetLeuTyrAlaArgThrThrSerLysProArgSerAlaSerGly 288
|||||
326 ACGACATGCTGTATGCACGAACACCCTCCAAAGCCCGCTCGGCTTCAGGA 277
|||||
289 AspThrValPheTrpGlyGluHisPheGluPheAsnAsnLeuProAlaVa 305
|||||
276 GACACCGTCTTTTGGGGCGGACGACTTTGAGTTTAAACAACCTGCCCTG 227
|||||
305 lArgAlaLeuArgLeuHisLeuTyrArgAspSerAspLysLysArgLysL 322
|||||
226 CCGGGCCCTTCGGCTGCATCTGTACCGTGAACCAAAAGCGGAAGA 177
|||||
322 ysAspLysAlaGlyTyrValGlyLeuValThrValProValAlaThrLeu 338
|||||
176 AGGACAAGGCTGGCTACGTTGGCCCTGGTGAAGTGTCCAGTGGCCACCTA 127
|||||
339 AlaGlyArgHisPheThrGluGlnTrpTyrProValThrLeuProThrG1 355
|||||
126 GCTGGGCGCCACTTCACAGACAGTGGTACCCCGTGAACCTTGGCCACAGG 77
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355 ySerGlyGlySerGlyGlyMetGlySerGlyGlyGlyGlySerGlyG 372
|||||
76 CAGTGGGGGCTCTGGGGGCGATGGGCTCGGGGGGAGGAGGGGTCCAGGG 27
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372 lGlySerGlyGlyLysGlyLysGly 380
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26 GTGGCTCAGGGGGCAAAAGGAAAGGA 1
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LOCUS      AW779747
DEFINITION      hn85f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3034699 3'
                similar to TR:095174 095174 NGAP. ;, mRNA sequence.
ACCESSION      AW779747
VERSION        AW779747.1 GI:7794350
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 593)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Tel: (301) 496-1550
                Email: Robert_Strausberg@nih.gov
                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                Emmert-Buck, M.D., Ph.D.
                CDNA Library Preparation: M. Bento Soares, Ph.D.
                CDNA Library Arrayed by: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL, send email to:
                info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:3034699"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT      104 a      169 c      178 g      141 t      1 others
ORIGIN
alignment_scores:
Quality: 737.50      Length: 217
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Percent Similarity: 82.028      Percent Identity: 63.594
alignment_block:
US-09-294-298-2 x AW779747/rev ..
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334 ProValAlaThrLeuAlaGly...ArgHisPheThrGluGlnTrpTyrPr 349
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593 CCTACCTGCTGCTCGGTGGCGCGCGAGTTCGTGGAGAGTGGTACCC 544
349 oValThrLeuProThrGlySerGlyGlySerGlyGlyMetGlySerGlyG 366
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543 GGTGTTGACGCCCAACCCCAAGGC..... 519
366 lyGlyGlyGlySerGlyGlyGlySerGlyGlyLysGlyLysGlyCys 382
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518 .....GGCAAGGGCACTGGA 504
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383 ProAlaValArgLeuLysAlaArgTyrGlnThrMetSerIleLeuProme 399
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503 CCCATGATCAGCATCAAGCGCGCTACCAAAACCATCACCATCTGCCCCAT 454
399 tGluLeuTyrLysGluPheAlaGluTyrValThrAsnHisTyrArgMetL 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
453 GGAGATGTACAAAGAGTTCGCTGAGCACATCACCAACCACTACCTGTGGC 404
416 euCysAlaValLeuGluProAlaLeuAsnValLysGlyLysGluGluVal 432
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403 TGTGTGAGCCCTCGAGCCCATCTCAGTGCCCAAGACCAAGGAGAGATG 354
433 AlaSerAlaLeuValHisIleLeuGlnSerThrGlyLysAlaLysAspPh 449
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
353 GCATCTGCCCTGGTGCACATCTGCAGAGCACGGGCAAGGTGAAGGACTT 304
449 eLeuSerAspMetAlaMetSerGluValAspArgPheMetGluArgGluH 466
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
303 CCTGACAGACCTGATGATGTCAGAGGTGGACCGCTGCGGGGACAAACGAGC 254
466 isLeuIlePheArgGluAsnThrLeuAlaThrLysAlaIleGluGluTyr 482
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
253 ACCTCATCTTCGGGGAGAACACACTGGCCACCAAGGCCATTGAGGAGTAC 204
483 MetArgLeuIleGlyGlnLysTyrLeuLysAspAlaIleGlyGluPheIl 499
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
203 CTCAAGCTAGTGGGCCAGAGTACNTGCAGGACGCCCTAGGTGAGTTTCA 154
499 eArgAlaLeuTyrGluSerGluGluAsnCysGluValAspProIleLysC 516
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
153 CAAAGCGCTGTATGAGTCAGATGAGAACTGCGAAGTGGATCCCAGCAAGT 104
516 yThrAlaSerSerLeuAlaGluHisGlnAlaAsnLeuArgMetCysCys 532
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
103 GCTCGCGCGCTGACCTCCAGAGACACAGGCCCAACCTCAAGATGTGCTGC 54
533 GluLeuAlaLeuCysLysValValAsnSerHisCysValPheProArgGl 549
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
53 GAGCTGGCGCTTCTGCAAGATCATCAACTCCTACTGTGTCTTCCCACGGGA 4
549 u 549
3 G 3
seq_name: gb_est44:AW421227
seq_documentation_block:      597 bp      mRNA      EST      09-FEB-2000
LOCUS      AW421227
DEFINITION      fj94f10.x1 zebrafish gridded kidney Danio rerio cDNA 3' similar to
                TR:095174 095174 NGAP. ;, mRNA sequence.
ACCESSION      AW421227
VERSION        AW421227.1 GI:6949159
KEYWORDS
SOURCE
ORGANISM      Danio rerio
                zebrafish.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE      1 (bases 1 to 597)
AUTHORS        Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
                ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
                ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
                Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
                Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                and Wilson,R.
TITLE          WashU Zebrafish EST Project 1998
JOURNAL        Unpublished (1998)
COMMENT        Other_ESTs: fj94f10.y1
                Contact: Stephen L. Johnson
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
```


